

Fig. 1

2020 TO 2020" SINESTRATION

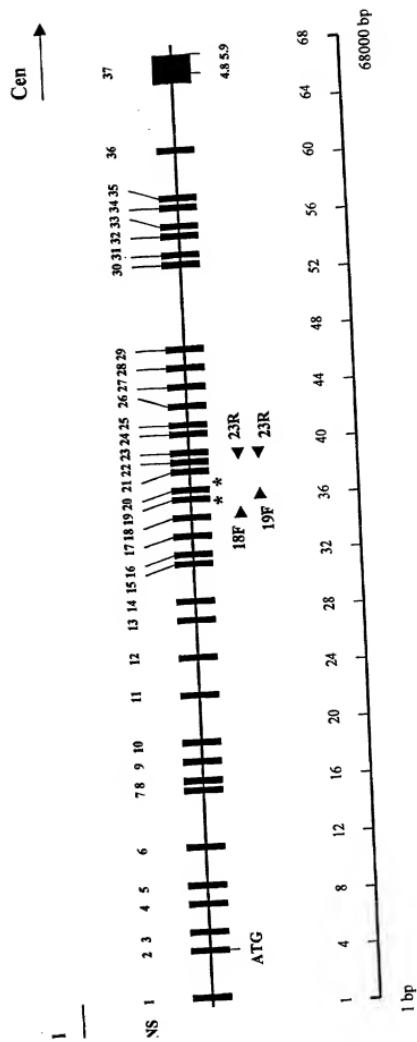


Fig. 2a



Fig. 2b

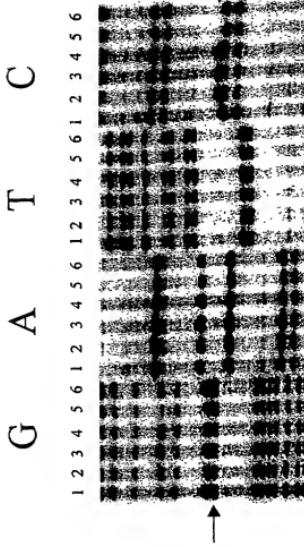


Fig. 3A

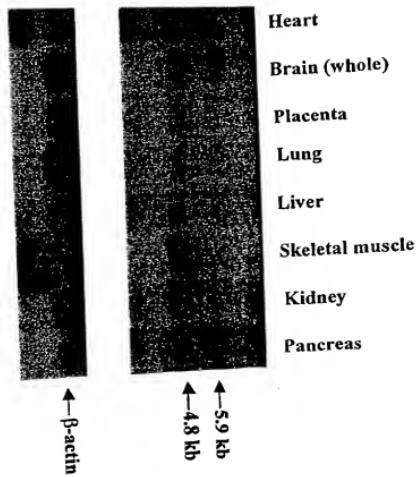


Fig. 3B

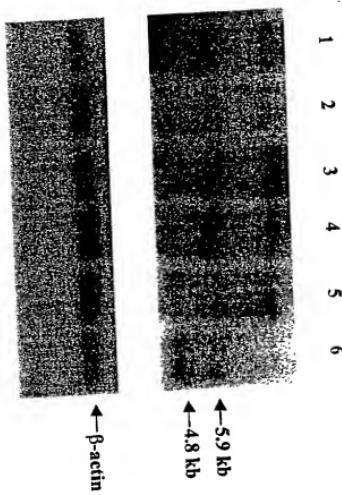


FIG. 4A

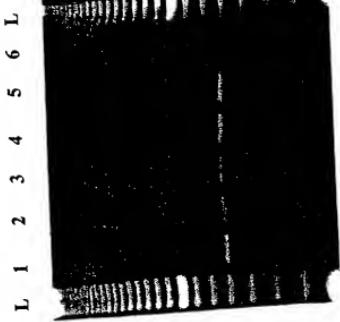


FIG. 4B

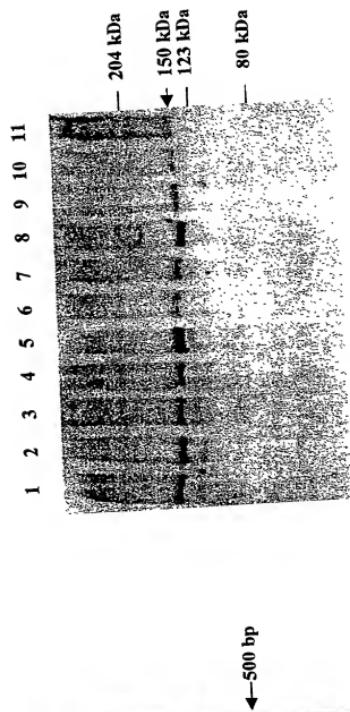




FIG. 5

FIGURE 6

IKBKAPgenomic.seq Length: 66479

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251 CTCAGGTAAG CGATCCATCC AGGGTAGGGG CACGGGAGTG GACCTCTCCG
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FIGURE 7

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Figure 7

Continued

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 3781 accccacggg caagagtc acatgttctc tgaatactgc agtgcgtga gtggcgtga
 3841 gatgatggc aataactccc atactaacttca gggatatac ccaagaatcg
 3901 ccgaaacggc gagccgaga agacgactgt caaaagacg agtccgtgg aggacgtgc
 3961 cctcttggag gcaactgtt aagtggtaa gacactgtt gaaactgaa aacctgaaag atgaatata
 4021 ccataatataa aagtaactt ttctttttt gtttgcgtt gaaactgaa aacccatgg
 4081 ggccatggaa gatgttgcg aagtttgcg ccagaattt ggacttttac
 4141 ttaccacg aattcagca ccccggtt aggttccaaat tctactgca atatgtatcat
 4201 ggcatcttat cagcaacaga agacttcgtt tccgtttttt gatgttgcg tttttatacc
 4261 accaaagatc aacaaatggc cccagttttt gctgagccgtt cttagactgt tgaactgcgt
 4321 tagggggat cccagacaga agacatttcc cacttttcc ttttttttttcc
 4381 ctcttttttggat gatgttgcg aagtttgcg ccagaattt ttccatggatt
 4441 gccaaggatc ttagacgaca aacaaacattt ctatattttt tttttttttt atatcatctt
 4501 atccatagca agacattaaat cttttttttt tttttttttt tttttttttt
 4561 ttccatcttgg gatgttgcg aactttttttt tttttttttt tttttttttt
 4621 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
 4681 cggagaaatc aatccatggc tttttttttt tttttttttt tttttttttt
 4741 ttccatcttgg tttttttttt tttttttttt tttttttttt tttttttttt
 4801 ttccatcttgg tttttttttt tttttttttt tttttttttt tttttttttt
 4861 gctgagccctt ctataatccaa atgttgcgtt gggactgtt tttttttttt tttttttttt
 4921 cttagatgtt gcaatgttgc tttttttttt tttttttttt tttttttttt
 4981 agttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
 5041 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
 5101 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
 5161 aaaactgtctt caaaatggaa atatttttt tttttttttt tttttttttt
 5221 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
 5281 gtatcttgc gcccattttt tttttttttt tttttttttt tttttttttt
 5341 gtgaaactt acctttttt acggatgtt gggcccccactt tttttttttt tttttttttt
 5401 tgaccacccat tttttttttt tttttttttt tttttttttt tttttttttt
 5461 gttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
 5521 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
 5581 agcaatgtt tttttttttt tttttttttt tttttttttt tttttttttt
 5641 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
 5701 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
 5761 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
 5821 tttttttttt tttttttttt tttttttttt tttttttttt tttttttttt
 5881 ctggaaatag aagttttttt tttttttttt tttttttttt tttttttttt

FIGURE 8

1 mnrnlklfrtl efrdiqqpgn pqcfslrteq gtvligsehg lievdpsvre vknevlvae
61 gflpedgsgr ivgvqdlldq esvcvatasg dvlclsstq qlecvgsvas gisvmswspd
121 qelvllatgq qtlimmtkdf epileqqihq nqdgfesqfit vwgkrketqf hgsegrqaaf
181 qmgmhesalp wddhrpqvtw rggqffavv vvcpetgark vrwnrefal qstsepavgl
241 gpalawkpsg sliastqdkp nqddivffek nglhhgftl pflkdevkvn dlwnadssv
301 lavrledigr ekssipktcv qlwtvgnhyw ylkqgslsfst cgkskivslm wdptvpyrlh
361 vlcqgwhyla ydwhwttdrs vgdnsdlsn vavidgnrwl vtvfrqtvvp ppmctyqlif
421 phpvnqvtfl ahpqksndla vldasmqsv ykcgdcpsad ptvklgavgg sqfkvcrltp
481 hlekrykifg ennedqdvnp edvflavshs efsprsvih ltaassemde
541 ehgqlnvss aavdgvisl ccnsktksvv lqladggifk ylwespslai kpwnksggfp
601 vrfpyptctq elamigeec vlgldrcrf findievasn itsfavydef lllttthshtc
661 qfcclrdasf ktlqaglssn hvshgevlrk vergsrrivtv vpqdtk1v1q mprgnlevvh
721 hralvlagir kwldklmfke afecmrklzi nlnpiydhnp kvflgnvtf ikqidsvnhi
781 nlfftelkee dvtktmypyap vtsvyslrd pdgnkidlvc damravmesi nphkyclsil
841 tshvkkttpe leivlqkvhe lqgnapsdpd avsaeealky llh1vdvnel ydhslgtyd
901 divlmvaeks qkdpkeylpf lntlkmetn yrftidkyl kryekaighl skcpeyfpe
961 cinlikdknl ynealklysp ssqyqydisi aygehlmgeh myepaglmfa rcahakals
1021 afitcgnwkq alcvaaqlnf tdkdqlvglr tlagklveq khidaamvle esaqdyeeav
1081 llllegawaee ealrlvkykn rldiietnwk psileaqkny mafldsqtat fscrhkrllv
1141 vrelkeqagg aglddevphg qesdlfsets svvsgsemgs kyshsnsris arssknrrka
1201 erkkhslkieg spledlalile alsevvqnte nlkdevyhil kvlflefde qgrelqafe
1261 dtqlmrsrl peiwtltyqq nsatpvlgn stansimasy qqktsvpv1 daelfippki
1321 nrرتqwkls1 ld

Figure 9

FIG. 1. Comparison of the amino acid sequence of Ikap across several species. Alignment of the amino acid sequence of Ikap (*M. musculus*) with that of *Homosapiens* (*H. sapiens*), *Drosophila melanogaster* (*D. melanogaster*), *Saccharomyces cerevisiae* (*S. cerevisiae*), *Arabidopsis thaliana* (*A. thaliana*), and *Caenorhabditis elegans* (*C. elegans*). Black boxes indicate identical AA, whereas conserved AA residues are shown in gray. Asterisk (*) at AA position 696 for mouse and human proteins indicates the location of the heterozygous R696G mutation found in only 4 PD patients. Sequence alignments were made using Pileup and Boxshade commands from GCG WISCONSIN Package 9.0 (Madison, WI).

Figure 9

Figure
Continued

Figure 9
Continued

TABLE 2. COMPARISON OF THE NOVEL MOUSE *Ikbbkap* GENE WITH MULTIPLE SPECIES HOMOLOGS

Species	Gene name	No. of amino acids	Molecular weight (kDa)	% aa identity with <i>M.m.</i>	GenBank Accession No.
<i>Mus musculus</i> (M.m.)	<i>Ikbbkap</i>	1332	149.11	—	AF367244
<i>Homo sapiens</i>	<i>IKBKA/P</i>	1332	149.11	80	AF153419
<i>Drosophila melanogaster</i>	<i>CG10335</i>	1213	138.21	32	AAF54670
<i>Saccharomyces cerevisiae</i>	<i>Epl1/Iki3p</i>	1349	152.99	29	AAB67278
<i>Arabidopsis thaliana</i>	Unknown	1308	146.63	27	BAB08695
<i>Caenorhabditis elegans</i>	Unknown	1177	134.80	24	AAF60430

Figure 10

140041356-010702

TABLE I. MOUSE *Ikbpap* EXON AND INTRON BOUNDARIES

Exon	Acceptor site	Donor site	Size (bp)	cDNA position
1		AGgtggatccgtcccg	129	1..129 ^a
2	ttttttccatcgAA	AAgtggatccgtatgc	163	130..292 ^b
3	tatgttttgcgtaaangGT	AGgtgggttgcggcc	153	293..445
4	ttttcgttgcgtacGCT	AGgttaatgttcgtacg*	82	446..527
5	acatgtacatccatcgCT	AGgttaatgttcgttgcg	81	528..608
6	cttggaaaatcgatgcC	TGgttaatgttcgtatgt	86	609..694
7	gggttttcttcgtatcgCC	TGgtttttcttcgtatcg*	97	695..791
8	cttaccccttgcgtatcgAG	AAgtttttatgtttatcgat*	91	792..882
9	agggttttgcgtatcgAC	AGgtttttatgtttatcgat	124	883..1006
10	ttttgtccatccatcgGT	TGgtttttatgtttatcgat	94	1007..1100
11	tccctccacacatcgTC	AAgtttttatgtttatcgat	231	1101..1331
12	ctttttatgttcgtatcgAC	TGgtttttatgtttatcgat	165	1332..1496
13	ttttttttttttttttttGT	TGgtttttatgtttatcgat	100	1497..1596
14	ctttttttttttttttttGT	AGgtttttatgtttatcgat	189	1597..1785
15	ctttttttttttttttttGT	GGgtttttatgtttatcgat	107	1786..1892
16	ttttttttttttttttttGT	AGgtttttatgtttatcgat	104	1893..1996
17	ttttttttttttttttttGT	AGgtttttatgtttatcgat	54	1997..2050
18	ttttttttttttttttttGT	AGgtttttatgtttatcgat	106	2051..2156
19	cactttttttttttttttTG	AGgtttttatgtttatcgat*	116	2157..2272
20	gggtttttttttttttttAT	AAgtttttatgtttatcgat*	74	2273..2346
21	tttttttttttttttttAT	AGgtttttatgtttatcgat	79	2347..2425
22	tttttttttttttttttAT	AGgtttttatgtttatcgat	80	2426..2505
23	tacttttttttttttttTG	AAgtttttatgtttatcgat	138	2506..2643
24	cactttttttttttttttGT	AGgtttttatgtttatcgat	86	2644..2729
25	ctttttttttttttttttGT	AGgtttttatgtttatcgat*	149	2730..2878
26	aactttttttttttttttGT	TGgtttttatgtttatcgat	124	2879..3002
27	ttttttttttttttttttGT	AGgtttttatgtttatcgat*	98	3003..3100
28	cgtttttttttttttttttGT	AGgtttttatgtttatcgat	202	3101..3302
29	tgtttttttttttttttttGT	AGgtttttatgtttatcgat	62	3303..3364
30	ctttttttttttttttttGT	TGgtttttatgtttatcgat	63	3365..3427
31	ttttttttttttttttttGT	AGgtttttatgtttatcgat*	61	3428..3488
32	attatgtttttttttttCC	GGgtttttatgtttatcgat*	114	3489..3602
33	gtttttttttttttttttAT	GCgtttttatgtttatcgat*	112	3603..3714
34	tgtttttttttttttttttGT	AGgtttttatgtttatcgat	128	3715..3842
35	ccatttttttttttttttGT	CGgtttttatgtttatcgat	155	3843..3997
36	cgtttttttttttttttGT	CGgtttttatgtttatcgat	76	3998..4073
37	cattttttttttttttttGT	CGgtttttatgtttatcgat	709	4074..4799 ^c

Figure 11

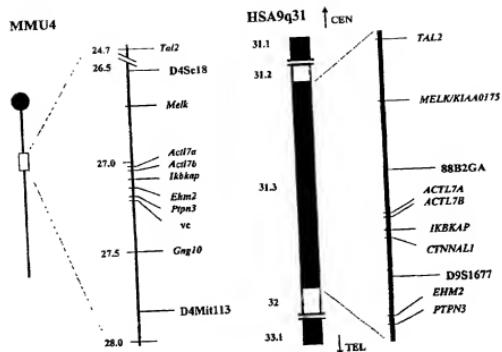


Figure 12